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SEQUENCE LISTING

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35 40 45

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

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<213> Mus musculus

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20 25 30

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35 40 45

Ala Ser Ile Ser Asp Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Asn Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr  
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Leu Gln Met Ser His Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys  
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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr  
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Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile  
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Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe  
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Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
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Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
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Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile  
65 70 75, 80

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20 25 30

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35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
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35 40 45

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro  
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Asp Arg Phe Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile

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70

75

80

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actagtcgac atgtatatat gtttgttgc tatttct 37

<210> 73

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Murine VL leader sequence forward primer

<400> 73  
actagtcgac atggaagccc cagctcagct tctttcc 38

<210> 74

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Murine VL leader sequence forward primer

<400> 74  
actagtcgac atgaagtttc cttctcaact tctgctc 37

<210> 75

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Murine gamma 1 constant region reverse primer

<400> 75  
ggatcccgaa ccagtggata gacagatg 28

<210> 76

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Murine gamma 2b constant region reverse primer

<400> 76  
ggatcccgaa agtggataga ctgatgg 27

<210> 77

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Murine kappa constant region reverse primer

<400> 77  
ggatccccggg tggatggtgg gaagatg 27

<210> 78

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> 2A10 VH forward primer

<400> 78  
actcataagg ttgccaccat gggatggagc tgtatcatcc tcttttggt ag 52

<210> 79

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> VH reverse primer

<400> 79  
actatgacta gtgtgccttg gccccagtag 30

<210> 80

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> VL forward primer

<400> 80  
actcataagg ttgccaccat gaggtgtct cttcagtttc tg 42

<210> 81  
<211> 29  
<212> DNA  
<213> Artificial sequence

<220>

<223> VL reverse primer  
<400> 81  
actatgcgta cgttcagct ccagcttgg

29

<210> 82  
<211> 19  
<212> PRT  
<213> Artificial sequence

<220>  
<223> CAMPATH-1H signal sequence  
<400> 82

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser

<210> 83  
<211> 120  
<212> PRT  
<213> Homo sapiens

<400> 83

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe  
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Gly Gln Trp Leu Val Ile Leu Asn Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 84 ..

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct H1

<400> 84

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser  
100 105 110

Ser

<210> 85

<211> 112

<212> PRT

<213> Homo sapiens

<400> 85

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly  
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Gly Leu Val Tyr Ser  
20 25 30

Asp Gly Asp Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser  
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly  
85 90 95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105 110

<210> 86

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VL construct L11

<400> 86

Asp Ile Val Ile Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly  
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys  
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu  
85 90 95

Val Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105 110

<210> 87

<211> 201

<212> PRT

<213> Homo sapiens

<400> 87

Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu  
1 5 10 15

Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu  
20 25 30

Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln  
35 40 45

Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile  
50 55 60

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val  
65 70 75 80

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu  
85 90 95

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile  
100 105 110

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro  
115 120 125

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro  
130 135 140

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val  
145 150 155 160

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp  
165 170 175

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu  
180 185 190

Ser Met Ile Glu Tyr Glu Asn Lys Glu  
195 200

<210> 88  
<211> 462  
<212> PRT  
<213> Artificial sequence

<220>  
<223> anti-NOGO antibody heavy chain  
<400> 88

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Met Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser  
85 90 95

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Leu Val  
115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
130 135 140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
165 170 175

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
180 185 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu  
195 200 205

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
210 215 220

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe  
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

385

390

395

400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
450 455 460

<210> 89

<211> 238

<212> PRT

<213> Artificial sequence

<220>

<223> anti-NOGO antibody light chain

<400> 89

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Asp Ile Val Ile Thr Gln Ser Pro Leu Ser Leu Pro Val  
20 25 30

Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu  
35 40 45

Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro  
50 55 60

Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser  
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Gly Ser Gly Thr Asp Phe Thr  
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys  
100 105 110

Gln Gln Leu Val Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu  
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala  
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 90

<211> 1428

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 88

<400> 90  
aagctttaca gttactcagc acacaggacc tcaccatggg atggagctgt atcatccctct 60  
tcttggttagc aacagctaca ggtgtccact cccaggtgca gctggtgca gtcggggctg 120

agggtgaagaa gcctggggcc tcagtgaagg tttcctgcaa ggcacatcgga tacaccctca	180
ccagctactg gatgcactgg gtgcgacagg cccctggaca agggctttag tggatggaa	240
atattaatcc tagcaatggt ggtactaact acaatgagaa gttcaagagc agagtcacca	300
tgaccaggga cacgtccacg agcacagtct acatggagct gagcagcctg agatctgagg	360
acacggccgt gtattactgt gaactggac agggctactg gggccaggaa acactagtca	420
cagtctccctc agcctccacc aaggcccatt cggtcttccc cctggcaccc tcctccaaga	480
gcacccctgg gggcacagcg gccctggct gcctggtcaa ggactacttc cccgaaccgg	540
tgcgggtgtc gtggaactca ggcccccata ccagcggcgt gcacacccctc ccggctgtcc	600
tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc agcagcttgg	660
gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag gtggacaaga	720
aagttgagcc caaatcttgc gacaaaactc acacatgccc accgtgcccc gcacctgaac	780
tcgcggggc accgtcagtc ttccctttcc ccccaaaacc caaggacacc ctcatgatct	840
cccgacccc tgaggtcaca tgcgtggtgg tggacgttag ccacgaagac cctgaggtca	900
agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag ccgcgggagg	960
agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtccctgcac caggactggc	1020
tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctccagcc cccatcgaga	1080
aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc ctgccccat	1140
cccggtatga gctgaccaag aaccaggtaa gcctgacctg cctggtaaaa ggcttctatc	1200
ccagcgcacat cgccgtggag tgggagagca atgggcagcc ggagaacaac tacaagacca	1260
cgccctccgt gctggactcc gacggctct tcttcctcta cagcaagctc accgtggaca	1320
agagcaggtg gcagcagggg aacgtttct catgctccgt gatgcattgag gctctgcaca	1380
accactacac gcagaagagc ctctccctgt ctccggtaa atgaattc	1428

<210> 91

<211> 758

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 89

<400> 91  
aagcttaca gttactcagc acacaggacc tcaccatggg atggagctgt atcatccctct 60  
tcttggttagc aacagctaca ggtgtccact ccgatattgt gataacccag tctccactct 120  
ccctgcccgt cacccttggga cagccggcct ccatctccctg caggtctagt aagagtctcc 180  
tatataagga tggaaagaca tacttgaatt ggttcagca gaggccaggc caatctccac 240  
agctcctaatttatttgatg tccacccgtg catctgggtt cccagacaga ttcagcggcg 300  
gtgggtcagg cactgatttc acactgaaaa tcagcagggt ggaggctgag gatgttgggg 360  
tttattactg ccaacaacctt gtagagtatc cgctcacgtt tggccagggg accaagctgg 420  
agatcaaacg tacggtggtgc gcaccatctg tcttcatctt cccgccccatct gatgagcagt 480  
tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc agagaggcca 540  
aagtacagtg gaaggtggac aacgcctcc aatcggttaa ctcccaggag agtgcacag 600  
agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg agcaaagcag 660  
actacgagaa acacaaagtc tacgcctgctg aagtcaccca tcagggcctg agctcgcccg 720  
tcacaaagag cttcaacagg ggagagtgtt aggaattc 758

<210> 92

<211> 462

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain sequence for HcLc

<400> 92

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys  
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser  
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
100 105 110

Tyr Tyr Cys Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Leu Val  
115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
130 135 140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
165 170 175

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
180 185 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu  
195 200 205

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
210 215 220

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
450 455 460

<210> 93

<211> 1405

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 92

<400> 93

aagcttgcca	ccatgggatg	gagctgtatac	atcctctttt	tggtagcagc	agctacaggt	60
gtccactccc	aggccaact	gcagcagcct	gggactgaac	tggtaagcc	tggggcttca	120
gtgaagctgt	cctgcaaggc	ttctggctac	accttcacca	gctactggat	gcactgggtg	180
aagcagaggc	ctggacaagg	ccttgagtgg	attggaaata	ttaatcctag	aatggtgtt	240
actaactaca	atgagaagtt	caagagcaag	gccacactga	ctgtagacaa	atcctccagc	300
acagcctaca	tgcagctcag	cagcctgaca	tctgaggact	ctgcggtcta	ttattgtgaa	360
ctgggacagg	gctactgggg	ccaaggcaca	ctagtcacag	tctcctcagc	ctccaccaag	420
ggcccatcg	tcttccccct	ggcacccctcc	tccaagagca	cctctggggg	cacagcggcc	480
ctgggctgcc	tggtaagga	ctacttcccc	gaaccggta	cggtgtcgtg	gaactcaggc	540
gccctgacca	gcggcgtgca	cacccccc	gctgtcctac	agtccctcagg	actctactcc	600
ctcagcagcg	tggtgaccgt	gcctccagc	agcttggca	cccagaccta	catctgcaac	660
gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaag	ttgagccaa	atcttgtgac	720
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tggggggacc	gtcagtcttc	780
ctcttcccc	caaaacccaa	ggacacccctc	atgatctccc	ggacccctga	ggtcacatgc	840
gtggtgtgg	acgtgagcca	cgaagacccct	gaggtcaagt	tcaactggta	cgtggacggc	900
gtggaggtgc	ataatgccaa	gacaaagccg	cgggaggagc	agtacaacag	cacgtaccgt	960
gtggtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	1020
aaggcttcca	acaaagccct	cccagccccc	atcgagaaaa	ccatctccaa	agccaaaggg	1080
cagccccgag	aaccacaggt	gtacacccctg	ccccatccc	ggatgagct	gaccaagaac	1140
caggtcagcc	tgacctgcct	ggtcaaaggc	ttctatccca	gcgacatcgc	cgtggagtgg	1200
gagagcaatg	ggcagccgga	gaacaactac	aagaccacgc	ctcccgctgct	ggactccgac	1260
ggctccttct	tcctctacag	caagctcacc	gtggacaaga	gcaggtggca	gcagggaaac	1320
gtctctcat	gtccgtgat	gcatgaggct	ctgcacaacc	actacacgca	gaagagcctc	1380
tccctgtctc	cgggtaaatg	aattc				1405

<210> 94  
<211> 239  
<212> PRT  
<213> Artificial sequence

<220>

<223> Light chain sequence for HcLc

<400> 94

Met Arg Cys Ser Leu Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser  
1 5 10 15

Gly Val Ser Gly Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro  
20 25 30

Val Thr Ser Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser  
35 40 45

Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg  
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala  
65 70 75 80

Ser Gly Val Ser Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe  
85 90 95

Thr Leu Glu Ile Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr  
100 105 110

Cys Gln Gln Leu Val Glu Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys  
115 120 125

Leu Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp

165

170

175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 95

<211> 738

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 94

<400> 95

aagcttgcca ccatgagggtg ctctcttcag tttctggggg tgcttatgtt ctggatctct	60
ggagtcagtg gggatattgt gataacccag gatgaactct ccaatcctgt cacttctgga	120
gaatcagttt ccatctccctg caggtcttagt aagagtctcc tatataagga tggaaagaca	180
tacctgaatt ggtttctgca gagaccagga caatctccctc agtcctgtat ctatttgatg	240
tccacccgtg catcaggagt ctcagaccgg ttttagtggca gtgggtcagg aacagatttc	300
accctggaaa tcagtagagt gaaggctgag gatgtgggtg tgtattactg tcaacaactt	360
gtagagtatc cgctcacgtt cggtgctggg accaagctgg agctgaaacg tacggtggt	420
gcaccatctg tcttcatctt cccgccatct gatgagcagt taaaaatctgg aactgcctct	480
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggac	540
aacgcctcc aatcggttaa ctcccaggag agtgtcacag agcaggacag caaggacagc	600
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc	660
tacgcctgctg aagtccaccca tcagggcctg agctcgcccc tcacaaagag cttcaacagg	720

ggagagtgtt aggaattc

738

<210> 96  
<211> 4  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif  
<400> 96  
Tyr Glu Asn Pro  
1

<210> 97  
<211> 4  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif  
<400> 97  
Lys Lys Gln Asn  
1